

Normal tissue exome-seq Tumor exome-seq QBRC somatic mutation calling pipeline

Missense mutations; Frameshift indels; Nonframeshift indels; Stoploss mutations

Binding affinity prediction (NetMHCpan, IEDB)

HLA-binding peptides

HLA typing (Athlates, OptiType)

HLA class I (A,B,C); HLA class II (DQB1, DRB1,3,4,5)

Tumor RNA-seq

Alignment (STAR); Expression counting (featureCounts); TCR identification (Mixcr, TRUST) Expression of exons and isoforms;
T cell receptor clones

Predicted neoantigens